

FIG. 1/

	TGGCTTCCCGTAGGTACCAGCAACCTGCTTCTGACTGGCCAG 412 SEQ.ID NO:315	371
370 2124	GGCAGCATACCAAGAAACTITGATGGCTACCGATCTCCGCTGCCCAATGAGAGCCAGCCCTCAGCCTTCTTCCCGAC	291 2125
290 2124	GGGACGTCGTGGGATCCGGAACTTCAGCGAGGGAAGCATCGAGACTCTGAGTAACAGCTCAGCTCCAGC GG-ACGTCGTGGGATCCGGACACAAAAAAAAAAAAAAAAA	211 2079
210 2078	GCGGCACATGTCCTCCATGCAGCACACGCAGGGGCCTCCGGGAGCGACTTGCCGACGCCATGGCCGAGTCACCTAGCC  GCGGCACATGTCCTCCATGGAGCACGCAGGGGGCTCCGGGAGCGACTTGCCGACGCCATGGCCGAGTCACCTAGCC  **********************************	131
130 1998	CGATCCTGGGGCCGAGGTACCTTTGACAGGAGCGTGACCCTGCTGGAGGTGTGCGGGAGCTGGCCTGAGGGTTTCGGGCT TGATGCTGCCTCAGGTACCTTTGACAGGAGCGTGACCCTGCTGGAGGTGTGCGGGAGCTGGCCTGAGGGCTTCGGGCT *** *** *** *** *** *** *************	51 1921
1920		1 1841
1840	AGICICATGGICGAGIGACACGCCACAGCCICITITIGGATITITIGATACAGAICITIGATCICAACAGAICICAGGATC	1761
1760	GATGGGTCCACAGTTCCAAAACCATCCCTCAGGCCAAACCACAGTTATCTCAGTTCAGTTCAGTTTCTTCTTCTTCTTCTTTTTCTTCTTCTTTTTTTT	1 1681
1680	GACCATAGTGGACAGGAAGAATGGCTTTCCCCAGGTTGAAATTGTAACACACAC	1601
1600	AGITICCIGCIIGCIIGGIIICCCCCIGGAAGIICCIGGGCCCCAITACICGACAIGGGICIITACGACAGIIITAGCIITCI	1 1521
1520	CCCTCAATGGAATGCAGCCACCGTTTAATGCAACCACCCTCTGCTCCTCGCTGCAGATGCAGTACAGTATTATC	1441
0 1440	1 1 AGCACTGCACCCAAGATTAGTGACGACACCACTGGAAATGATGACATCGCCTCGAGCCAGCTGGACTCTGGAAC	1361
1360	1 1 AACAAGITIGIAGITIGAGICCCIGIACAITIAICAGITIGCIAIGGCACCITIAGIGGAACACAIGAIGGAGCCGCGACCCTIC	1281

## FIG. 1B

80	70 160	150 240	230	6 300 400	300 480	300	300 640	300	300 800	300 880	300 960	300 1040	300	300	300	300	
1 1 CGACIAACTICTICAGITAACAGCTICCACCAGCGGGGGGCATACCAAGAAACTTTIGATGGCTACCGATCTICCGCTGCCC	1 81 ACCAATGAGAGCCCCCTCAGCCTCTTCCCGACTGGCTTCCCGTAGGTACCAGCAACCTGCTTCTGACTGGCCAGCCC  82 ACCAATGAGAGCCAGCCCCTCTTCCCGACTGGCTTCCCGTAGGTACCAGCAACCTGCTTCTGACTGGCCAGCCC  83 ACCAATGAGAGCCAGCCCCTCTTCCCGACTGGCTTCCCGTAGGTACCAGCAACCTGCTTCTGACTGGCCAGCCC  84 A A A A A A A A A A A A A A A A A A A	71 CCTCCCCTGCTGCAGGAGGAGAAGCCCCCGCTCTGGTCCTTCAGTCTCTGCTCTTCCTTTCATCAACCACCTTCC 61 CCTCCCCTGCTGCAGGAGGAAAAAAAAAAAAAAAAAAAA	1 CCAAGCTTA( *********	H	<del>, -  - </del>	11 GGGGCCTGAGTGGGGACAGAGTTGATCGTCCACCTGGCCATTTTGACCCTGAGTGGACAGTCACAGCCTCAGCTCATGT	1 51 CIGGIGIGACACACACIGCCCCCAGCITCCCITIGGTCAGCCCCAACTCCAGCGGGGTGAACGGAGGCCCAGAGTACTA	11 GGGAAGGAAGGAAGACATGCCTCTTCTTCTTTCCTCCCCATCTGTTCCTGGAAGAGTTTGTTT	301 721 CITIPAGCCCCITITACCCIGGICATGAICAGIGAAGGAAACCGIGGITACIGAGGCCCIGIIGAAAAAGIGCACGI	01 01 CITGICCAATAAATCACGCIGCAGAAAAAAAAAAAAAAAA	301 881 CCCTTTAGTGAGGGTTAATTTTAGCTTGGCACTGGTCGTTTTTACAACGTCGTGGTAAACCTGGCGTTAAACCTTGGCGTTTACCAA	15. 51 ACTIVATOGEOTIGEAGEACATECECECTITICGECTGGEGTAATAGEGAAGAGGECEGEACEGATEGECATITICECTAACAACAA	1 11 AGTIYGCGCAGCCIYGAAIYGGCAATYGGCGCCCCTGIAGCGCGCGCCATTAAGCGCGCGGGGTGIYGGTTACCGCGCAAG	1 CGIGACCGCIACACITIGCCAGCGCCCCIAGCGCCCCGCITITICGCITICCITIC	01 01 TITCCCCCCTCAAGCTCTAAATCGGGGGCTCCCCTTTAGGGTTCCCGATITTAGTGCTTTTACCGGCACCTCGACCCCAAAA	01 81 AACTIGATTAGGGTGATGGTTCACGTAGTGGCCCATCGCCCTGATAAGACGGTTTTTCGCCCTTTGACGTTCGAGTCCAC	61 GITCT 1365 SEQ. ID NO:318 FIG. 2
	$\omega$	16	15 24	23	30	30 48 80	301 561	301 641	73(	301 801	ñã	930	30	30	3(	128	13(

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